



## RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/889,344A  
Source: OIPB  
Date Processed by STIC: 7-22-02

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: [patin21help@uspto.gov](mailto:patin21help@uspto.gov) or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: [patin3help@uspto.gov](mailto:patin3help@uspto.gov) or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.1 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: U.S. Patent and Trademark Office, Box Sequence, P.O. Box 2327, Arlington, VA 22202
3. Hand Carry directly to:  
U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7<sup>th</sup> Floor, Examiner Name, Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202  
Or  
U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

# Raw Sequence Listing Error Summary

## ERROR DETECTED

## SUGGESTED CORRECTION

SERIAL NUMBER: 09/889344

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1      Wrapped Nucleics  
    Wrapped Aminos  
The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2      Invalid Line Length  
The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3      Misaligned Amino  
    Numbering  
The numbering under each 5<sup>th</sup> amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4      Non-ASCII  
The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5      Variable Length  
Sequence(s)      contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6      PatentIn 2.0  
    "bug"  
A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s)     . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7      Skipped Sequences  
    (OLD RULES)  
Sequence(s)      missing. If intentional, please insert the following lines for each skipped sequence:  
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)  
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
This sequence is intentionally skipped  
  
Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8      Skipped Sequences  
    (NEW RULES)  
Sequence(s)      missing. If intentional, please insert the following lines for each skipped sequence.  
<210> sequence id number  
<400> sequence id number  
000
- 9      Use of n's or Xaa's  
    (NEW RULES)  
Use of n's and/or Xaa's have been detected in the Sequence Listing.  
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.  
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10      Invalid <213>  
    Response  
Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11      Use of <220>  
Sequence(s)      missing the <220> "Feature" and associated numeric identifiers and responses.  
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.  
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12      PatentIn 2.0  
    "bug"  
Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13      Misuse of n  
n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

## Raw Sequence Listing Error Summary .

### ERROR DETECTED      SUGGESTED CORRECTION

SERIAL NUMBER: 09/889,344A

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1      Wrapped Nucleics      The number/text at the end of each line "wrapped" down to the next line. This may occur if your file  
     Wrapped Aminos      was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will  
     prevent "wrapping."
  
- 2      Invalid Line Length      The rules require that a line not exceed 72 characters in length. This includes white spaces.
  
- 3      Misaligned Amino      The numbering under each 5<sup>th</sup> amino acid is misaligned. Do not use tab codes between numbers;  
     Numbering      use space characters, instead.
  
- 4      Non-ASCII      The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please  
     ensure your subsequent submission is saved in ASCII text.
  
- 5      Variable Length      Sequence(s)      contain n's or Xaa's representing more than one residue. Per Sequence Rules,  
     each n or Xaa can only represent a single residue. Please present the maximum number of each  
     residue having variable length and indicate in the <220>-<223> section that some may be missing.
  
- 6      PatentIn 2.0      A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid  
     "bug"      sequences(s)     . Normally, PatentIn would automatically generate this section from the  
     previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to  
     the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for  
     Artificial or Unknown sequences.
  
- 7      Skipped Sequences      Sequence(s)      missing. If intentional, please insert the following lines for each skipped sequence:  
     (OLD RULES)      (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
     (i)      SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)  
     (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
     This sequence is intentionally skipped  
  
     Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
  
- 8      Skipped Sequences      Sequence(s)      missing. If intentional, please insert the following lines for each skipped sequence.  
     (NEW RULES)      <210> sequence id number  
     <400> sequence id number  
     000
  
- 9      Use of n's or Xaa's      Use of n's and/or Xaa's have been detected in the Sequence Listing.  
     (NEW RULES)      Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.  
     In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
  
- 10      Invalid <213>      Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or  
     Response      scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or  
     is Artificial Sequence
  
- 11      ✓ Use of <220>      Sequence(s)      missing the <220> "Feature" and associated numeric identifiers and responses.  
     Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or  
     "Unknown." Please explain source of genetic material in <220> to <223> section.  
     (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
  
- 12      PatentIn 2.0      Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file,  
     "bug"      resulting in missing mandatory numeric identifiers and responses (as indicated in raw sequence  
     listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

Does Not Comply  
Corrected Diskette Needed



OIKE

## RAW SEQUENCE LISTING

DATE: 07/22/2002

PATENT APPLICATION: US/09/889,344A

TIME: 10:40:33

Input Set : A:\USSEQLIST2.txt

Output Set: N:\CRF3\07222002\I889344A.raw

```

4 <110> APPLICANT: CHEN, WENFANG
5      MEEK, THOMAS D.
6      POWELL, DAVID J.
7      TEW, DAVID G.
10 <120> TITLE OF INVENTION: Method of Site Specific Labeling of Proteins and Uses
11      Therefor
14 <130> FILE REFERENCE: P50892
16 <140> CURRENT APPLICATION NUMBER: 09/889,344A
17 <141> CURRENT FILING DATE: 2001-07-16
19 <150> PRIOR APPLICATION NUMBER: PCT/US00/01481
20 <151> PRIOR FILING DATE: 2000-01-20
22 <150> PRIOR APPLICATION NUMBER: US 60/117,327
23 <151> PRIOR FILING DATE: 1999-01-22
25 <160> NUMBER OF SEQ ID NOS: 16
27 <170> SOFTWARE: FastSEQ for Windows Version 3.0
29 <210> SEQ ID NO: 1
30 <211> LENGTH: 5
31 <212> TYPE: PRT
32 <213> ORGANISM: Artificial Sequence
34 <220> FEATURE:
35 <221> NAME/KEY: unsure
36 <222> LOCATION: (5)
37 <223> OTHER INFORMATION: Where Xaa at position (5) can represent Leucine or Isoleucine
39 <400> SEQUENCE: 1
W--> 40  Gln Ser Lys Val Xaa
41      1          5
43 <210> SEQ ID NO: 2
44 <211> LENGTH: 207
45 <212> TYPE: PRT
46 <213> ORGANISM: Artificial Sequence
48 <220> FEATURE:
49 <221> NAME/KEY: unsure
50 <222> LOCATION: (1)(2)(3)(4)(5)(6)(7)(8)(9)(10)(11)(12)(13)(14)(15)
51 <222> LOCATION: (16)(17)(18)(19)(20)(21)(22)(23)(24)(25)(26)(27)(28)
W--> 52 <222> (29)(30)(31)(32)(33)(34)(35)(36)(37)(38)(39)(40)(41)
W--> 53 <222> (42)(43)(44)(45)(46)(47)(48)(49)(50)(51)(52)(53)(54)
W--> 54 <222> (55)(56)(57)(58)(59)(60)(61)(62)(62)(64)(65)(66)(67)
W--> 55 <222> (68)(69)(70)(71)(72)(73)(74)(75)(76)(77)(78)(79)(80)
W--> 56 <222> (81)(82)(83)(84)(85)(86)(87)(88)(89)(90)(91)(92)(93)
W--> 57 <222> (94)(95)(96)(97)(98)(99)(100)(101)(106)(107)(108)(109)
W--> 58 <222> (110)(111)(112)(113)(114)(115)(116)(117)(118)(119)(120)
W--> 59 <222> (121)(122)(123)(124)(125)(126)(127)(128)(129)(130)(131)
W--> 60 <222> (132)(133)(134)(135)(136)(137)(138)(139)(140)(141)(142)

```

See Item # 11 on ERROR  
Summary SHEET

## RAW SEQUENCE LISTING

DATE: 07/22/2002

PATENT APPLICATION: US/09/889,344A

TIME: 10:40:33

Input Set : A:\USSEQLIST2.txt

Output Set: N:\CRF3\07222002\I889344A.raw

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W--> 61 <222> (143)(144)(145)(146)(147)(148)(149)(150)(151)(152)(153)
W--> 62 <222> (154)(155)(156)(157)(158)(159)(160)(161)(162)(163)(164)
W--> 63 <222> (165)(166)(167)(168)(169)(170)(171)(172)(173)(174)(175)
W--> 64 <222> (176)(177)(178)(179)(180)(181)(182)(183)(184)(185)(186)
W--> 65 <222> (187)(188)(189)(190)(191)(192)(193)(194)(195)(196)(197)
W--> 66 <222> (198)(199)(200)(201)(202)(203)(204)(205)(206)(207)
67 <223> OTHER INFORMATION: Where Xaa can represent none or any one of the twenty
naturally
68 <223> OTHER INFORMATION: occurring amino acids
W--> 70 <400> 2
W--> 71 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
72 1 5 10 15
W--> 73 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
74 20 25 30
W--> 75 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
76 35 40 45
W--> 77 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
78 50 55 60
W--> 79 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
80 65 70 75 80
W--> 81 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
82 85 90 95
W--> 83 Xaa Xaa Xaa Xaa Xaa Gln Ser Lys Val Xaa Xaa Xaa Xaa Xaa Xaa Xaa
84 100 105 110
W--> 85 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
86 115 120 125
W--> 87 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
88 130 135 140
W--> 89 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
90 145 150 155 160
W--> 91 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
92 165 170 175
W--> 93 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
94 180 185 190
W--> 95 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
96 195 200 205
98 <210> SEQ ID NO: 3
99 <211> LENGTH: 207
100 <212> TYPE: PRT
101 <213> ORGANISM: Artificial Sequence
103 <220> FEATURE:
104 <221> NAME/KEY: unsure
105 <222> LOCATION: (1)(2)(3)(4)(5)(6)(7)(8)(9)(10)(11)(12)(13)(14)(15)
106 <222> LOCATION: (16)(17)(18)(19)(20)(21)(22)(23)(24)(25)(26)(27)(28)
W--> 107 <222> (29)(30)(31)(32)(33)(34)(35)(36)(37)(38)(39)(40)(41)
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W--> 110 <222> (68)(69)(70)(71)(72)(73)(74)(75)(76)(77)(78)(79)(80)
W--> 111 <222> (81)(82)(83)(84)(85)(86)(87)(88)(89)(90)(91)(92)(93)
W--> 112 <222> (94)(95)(96)(97)(98)(99)(100)(101)(106)(107)(108)(109)

```

See item # 11 on  
ERROR SUMMARY SHEET

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Input Set : A:\USSEQLIST2.txt

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W--> 113 <222> (110)(111)(112)(113)(114)(115)(116)(117)(118)(119)(120)
W--> 114 <222> (121)(122)(123)(124)(125)(126)(127)(128)(129)(130)(131)
W--> 115 <222> (132)(133)(134)(135)(136)(137)(138)(139)(140)(141)(142)
W--> 116 <222> (143)(144)(145)(146)(147)(148)(149)(150)(151)(152)(153)
W--> 117 <222> (154)(155)(156)(157)(158)(159)(160)(161)(162)(163)(164)
W--> 118 <222> (165)(166)(167)(168)(169)(170)(171)(172)(173)(174)(175)
W--> 119 <222> (176)(177)(178)(179)(180)(181)(182)(183)(184)(185)(186)
W--> 120 <222> (187)(188)(189)(190)(191)(192)(193)(194)(195)(196)(197)
W--> 121 <222> (198)(199)(200)(201)(202)(203)(204)(205)(206)(207)
122 <223> OTHER INFORMATION: Where Xaa can represent none or any one of the twenty
naturally
123 <223> OTHER INFORMATION: occurring amino acids
W--> 125 <400> 3
W--> 126 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
127 1 5 10 15
W--> 128 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
129 20 25 30
W--> 130 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
131 35 40 45
W--> 132 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
133 50 55 60
W--> 134 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
135 65 70 75 80
W--> 136 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
137 85 90 95
W--> 138 Xaa Xaa Xaa Xaa Xaa Gln Ser Lys Val Xaa Xaa Xaa Xaa Xaa Xaa Xaa
139 100 105 110
W--> 140 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
141 115 120 125
W--> 142 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
143 130 135 140
W--> 144 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
145 145 150 155 160
W--> 146 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
147 165 170 175
W--> 148 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
149 180 185 190
W--> 150 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
151 195 200 205
153 <210> SEQ ID NO: 4
154 <211> LENGTH: 10
155 <212> TYPE: PRT
156 <213> ORGANISM: Artificial Sequence
158 <220> FEATURE:
159 <223> OTHER INFORMATION: Derivative of a factor XIII substrate
161 <400> SEQUENCE: 4
162 Leu Ser Leu Ser Gln Ser Lys Val Leu Gly
163 1 5 10
165 <210> SEQ ID NO: 5
166 <211> LENGTH: 10

```

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Input Set : A:\USSEQLIST2.txt

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```

167 <212> TYPE: PRT
168 <213> ORGANISM: Artificial Sequence
170 <220> FEATURE:
171 <223> OTHER INFORMATION: Derivative of a factor XIII substrate
173 <400> SEQUENCE: 5
174   Ile Gly Glu Gly Gln Ser Lys Val Leu Gly
175     1             5             10
177 <210> SEQ ID NO: 6
178 <211> LENGTH: 10
179 <212> TYPE: PRT
180 <213> ORGANISM: Artificial Sequence
182 <220> FEATURE:
183 <223> OTHER INFORMATION: Derivative of a factor XIII substrate
185 <400> SEQUENCE: 6
186   Leu Gly Pro Gly Gln Ser Lys Val Ile Gly
187     1             5             10
189 <210> SEQ ID NO: 7
190 <211> LENGTH: 81
191 <212> TYPE: DNA
192 <213> ORGANISM: Unknown
194 <220> FEATURE:
195 <223> OTHER INFORMATION: Oligonucleotide designed to introduce Q tag
197 <400> SEQUENCE: 7
198   tgtacctcag accatatgag cctgtccctg tcccagtcca aagttctgcc ggggccgagc      60
199   actatcgaag aacgcgttaa g                                     81
201 <210> SEQ ID NO: 8
202 <211> LENGTH: 37
203 <212> TYPE: DNA
204 <213> ORGANISM: Unknown
206 <220> FEATURE:
207 <223> OTHER INFORMATION: Oligonucleotide designed to introduce Q tag
209 <400> SEQUENCE: 8
210   tgatgtcagt caagcttacg cctgggtggcc gttgatg      37
212 <210> SEQ ID NO: 9
213 <211> LENGTH: 14
214 <212> TYPE: PRT
215 <213> ORGANISM: Artificial Sequence
217 <220> FEATURE:
218 <223> OTHER INFORMATION: Derivative of a factor XIII substrate
220 <400> SEQUENCE: 9
221   Met Ser Leu Ser Leu Ser Gln Ser Lys Val Leu Pro Gly Pro
222     1             5             10
224 <210> SEQ ID NO: 10
225 <211> LENGTH: 37
226 <212> TYPE: DNA
227 <213> ORGANISM: Unknown
229 <220> FEATURE:
230 <223> OTHER INFORMATION: Oligonucleotide designed to introduce Q tag
232 <400> SEQUENCE: 10

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## RAW SEQUENCE LISTING

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PATENT APPLICATION: US/09/889,344A

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Input Set : A:\USSEQLIST2.txt

Output Set: N:\CRF3\07222002\I889344A.raw

```

233  tgtacctcag accatatgag cactatcgaa gaacgcg          37
235 <210> SEQ ID NO: 11
236 <211> LENGTH: 78
237 <212> TYPE: DNA
238 <213> ORGANISM: Unknown
240 <220> FEATURE:
241 <223> OTHER INFORMATION: Oligonucleotide designed to introduce Q tag
243 <400> SEQUENCE: 11
244  tgatgtcagt caagcttacg gaccgcgcag aactttggac tgggacaggg acagcgctg          60
245  gtggccgttg atgtaatc                                     78
247 <210> SEQ ID NO: 12
248 <211> LENGTH: 12
249 <212> TYPE: PRT
250 <213> ORGANISM: Artificial Sequence
252 <220> FEATURE:
253 <223> OTHER INFORMATION: Derivative of E. coli ACP protein
255 <400> SEQUENCE: 12
256  Leu Ser Leu Ser Gln Ser Lys Val Leu Pro Gly Pro
257    1           5              10
259 <210> SEQ ID NO: 13
260 <211> LENGTH: 92
261 <212> TYPE: DNA
262 <213> ORGANISM: Unknown
264 <220> FEATURE:
265 <223> OTHER INFORMATION: Oligonucleotide designed to introduce Q tag into
266   Streptococcus haemophilus FabH gene
268 <400> SEQUENCE: 13
269  tatcatatga gcctgtccct gtcccagtc aaagttctgc cgggtccggg taccctcgag          60
270  ggatccgctt ttgcaaaaat aagtcagggt gc                                     92
272 <210> SEQ ID NO: 14
273 <211> LENGTH: 53
274 <212> TYPE: DNA
275 <213> ORGANISM: Unknown
277 <220> FEATURE:
278 <223> OTHER INFORMATION: Oligonucleotide designed to introduce Q tag into
279   Streptococcus haemophilus FabH gene
281 <400> SEQUENCE: 14
282  ctcagatctg agctcactag tggatcctta aattgtaaga atgagcgtgc ccc          53
284 <210> SEQ ID NO: 15
285 <211> LENGTH: 364
286 <212> TYPE: PRT
287 <213> ORGANISM: Artificial Sequence
289 <220> FEATURE:
290 <223> OTHER INFORMATION: Modified sequence of Streptococcus haemophilus FabH
292 <400> SEQUENCE: 15
293  Met Gly His His His His His His His His His Ser Ser Gly His
294    1           5              10              15
295  Ile Glu Gly Arg His Met Ser Leu Ser Leu Ser Gln Ser Lys Val Leu
296    20          25              30

```



RAW SEQUENCE LISTING ERROR SUMMARY      DATE: 07/22/2002  
PATENT APPLICATION:    US/09/889,344A      TIME: 10:40:34

Input Set : A:\USSEQLIST2.txt  
Output Set: N:\CRF3\07222002\I889344A.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:1; Xaa Pos. 5  
Seq#:2; Xaa Pos. 1,2,3,4,5,6,7,8,9,10,11,12,13,14,15,16,17,18,19,20,21,22  
Seq#:2; Xaa Pos. 23,24,25,26,27,28,29,30,31,32,33,34,35,36,37,38,39,40,41  
Seq#:2; Xaa Pos. 42,43,44,45,46,47,48,49,50,51,52,53,54,55,56,57,58,59,60  
Seq#:2; Xaa Pos. 61,62,63,64,65,66,67,68,69,70,71,72,73,74,75,76,77,78,79  
Seq#:2; Xaa Pos. 80,81,82,83,84,85,86,87,88,89,90,91,92,93,94,95,96,97,98  
Seq#:2; Xaa Pos. 99,100,101,106,107,108,109,110,111,112,113,114,115,116,117  
Seq#:2; Xaa Pos. 118,119,120,121,122,123,124,125,126,127,128,129,130,131  
Seq#:2; Xaa Pos. 132,133,134,135,136,137,138,139,140,141,142,143,144,145  
Seq#:2; Xaa Pos. 146,147,148,149,150,151,152,153,154,155,156,157,158,159  
Seq#:2; Xaa Pos. 160,161,162,163,164,165,166,167,168,169,170,171,172,173  
Seq#:2; Xaa Pos. 174,175,176,177,178,179,180,181,182,183,184,185,186,187  
Seq#:2; Xaa Pos. 188,189,190,191,192,193,194,195,196,197,198,199,200,201  
Seq#:2; Xaa Pos. 202,203,204,205,206,207  
Seq#:3; Xaa Pos. 1,2,3,4,5,6,7,8,9,10,11,12,13,14,15,16,17,18,19,20,21,22  
Seq#:3; Xaa Pos. 23,24,25,26,27,28,29,30,31,32,33,34,35,36,37,38,39,40,41  
Seq#:3; Xaa Pos. 42,43,44,45,46,47,48,49,50,51,52,53,54,55,56,57,58,59,60  
Seq#:3; Xaa Pos. 61,62,63,64,65,66,67,68,69,70,71,72,73,74,75,76,77,78,79  
Seq#:3; Xaa Pos. 80,81,82,83,84,85,86,87,88,89,90,91,92,93,94,95,96,97,98  
Seq#:3; Xaa Pos. 99,100,101,106,107,108,109,110,111,112,113,114,115,116,117  
Seq#:3; Xaa Pos. 118,119,120,121,122,123,124,125,126,127,128,129,130,131  
Seq#:3; Xaa Pos. 132,133,134,135,136,137,138,139,140,141,142,143,144,145  
Seq#:3; Xaa Pos. 146,147,148,149,150,151,152,153,154,155,156,157,158,159  
Seq#:3; Xaa Pos. 160,161,162,163,164,165,166,167,168,169,170,171,172,173  
Seq#:3; Xaa Pos. 174,175,176,177,178,179,180,181,182,183,184,185,186,187  
Seq#:3; Xaa Pos. 188,189,190,191,192,193,194,195,196,197,198,199,200,201  
Seq#:3; Xaa Pos. 202,203,204,205,206,207

## VERIFICATION SUMMARY

DATE: 07/22/2002

PATENT APPLICATION: US/09/889,344A

TIME: 10:40:34

Input Set : A:\USSEQLIST2.txt

Output Set: N:\CRF3\07222002\I889344A.raw

L:40 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:0  
L:52 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:2  
L:53 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:2  
L:54 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:2  
L:55 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:2  
L:56 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:2  
L:57 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:2  
L:58 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:2  
L:59 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:2  
L:60 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:2  
L:61 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:2  
L:62 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:2  
L:63 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:2  
L:64 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:2  
L:65 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:2  
L:66 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:2  
L:70 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:2  
L:71 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2 after pos.:0  
L:73 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2 after pos.:16  
L:75 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2 after pos.:32  
L:77 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2 after pos.:48  
L:79 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2 after pos.:64  
L:81 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2 after pos.:80  
L:83 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2 after pos.:96  
L:85 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2 after pos.:112  
L:87 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2 after pos.:128  
L:89 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2 after pos.:144  
L:91 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2 after pos.:160  
L:93 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2 after pos.:176  
L:95 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2 after pos.:192  
L:107 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:3  
L:108 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:3  
L:109 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:3  
L:110 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:3  
L:111 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:3  
L:112 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:3  
L:113 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:3  
L:114 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:3  
L:115 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:3  
L:116 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:3  
L:117 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:3  
L:118 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:3  
L:119 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:3  
L:120 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:3  
L:121 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:3  
L:125 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:3  
L:126 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:0  
L:128 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:16

## VERIFICATION SUMMARY

DATE: 07/22/2002

PATENT APPLICATION: US/09/889,344A

TIME: 10:40:34

Input Set : A:\USSEQLIST2.txt

Output Set: N:\CRF3\07222002\I889344A.raw

L:130 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:32  
L:132 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:48  
L:134 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:64  
L:136 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:80  
L:138 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:96  
L:140 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:112  
L:142 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:128  
L:144 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:144  
L:146 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:160  
L:148 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:176  
L:150 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:192